

Db 371 VTTYKLIVINGKTLKGETTTEAVDAATAEKVKQYANDNGVDGWTYDDATKTFTVTE 427

RESULT 4

SPG1_STRSG STANDARD; PRT; 448 AA.

AC P06654;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Immunoglobulin G binding protein G precursor (IgG binding protein G).

GN Name=spg;

OS Streptococcus sp. (Lancefield group G).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1320;

RN [1]

RP SEQUENCE FROM N.A. PubMed=3745123;

RX MEDLINE=86304178; PubMed=3745123;

RA Fahnestock S.R., Alexander P., Nagle J., Filpula D.;

RT "Gene for an immunoglobulin-binding protein from a group G streptococcus.";

RL J. Bacteriol. 167:870-880(1986).

RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS) OF 228-282.

RX MEDLINE=94213848; PubMed=8161530;

RA Gallagher T., Alexander P., Bryan P., Gilliland G.L.;

RT "Two crystal structures of the B1 immunoglobulin-binding domain of streptococcal protein G and comparison with NMR.";

RL Biochemistry 33:4721-4729(1994).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS) OF 293-351.

RX MEDLINE=95055731; PubMed=7966308;

RA Derrick J.P., Wigley D.B.;

RT "The third IgG-binding domain from streptococcal protein G. An analysis by X-ray crystallography of the structure alone and in a complex with Fab.";

RL J. Mol. Biol. 243:906-918(1994).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 297-352.

RX MEDLINE=95308043; PubMed=7788293; DOI=10.1016/S0969-2126(01)00157-5;

RA Sauer-Eriksson A.B., Kleywegt G.J., Uhlen M., Jones T.A.;

RT "Crystal structure of the C2 fragment of streptococcal protein G in complex with the Fc domain of human IgG.";

RL Structure 3:265-278(1995).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS) OF 228-282.

RA Butterworth S., Lamzin V.S., Wigley D.B., Derrick J.P., Wilson K.S.;

RL Submitted (APR-1997) to the PDB data bank.

RN [6]

RP STRUCTURE BY NMR OF 298-351.

RX MEDLINE=91335209; PubMed=1871600;

RA Gronenborn A.M., Filpula D.R., Essig N.Z., Achari A., Whitlow M., Wingfield P.T., Clore G.M.;

RT "A novel, highly stable fold of the immunoglobulin binding domain of streptococcal protein G.";

RL Science 253:657-661(1991).

CC -!- FUNCTION: Binds to the constant Fc region of IgG with high affinity.

CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).

CC -----

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CC -----

DR EMBL; M13825; AAA03664.1; --

DR PIR; A24496; A24496.

DR PDB; 1EM7; X-ray; A=227-282.

DR PDB; 1FCC; X-ray; --

DR PDB; 1GB1; NMR; @=227-282.

DR PDB; 1IGC; X-ray; A=292-352.

DR PDB; 1IGD; X-ray; @=292-352.

DR PDB; 1MPE; NMR; A/B/C/D=227-282.

DR PDB; 1MVK; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=227-282.

DR PDB; 1PGA; X-ray; @=227-282.

DR PDB; 1PGB; X-ray; @=227-282.

DR PDB; 1PGX; X-ray; @=284-366.

DR PDB; 1Q10; NMR; A/B=227-282.

DR PDB; 2GB1; NMR; @=227-282.

DR PDB; 2IGD; X-ray; @=292-352.

DR PDB; 2IGH; NMR; @=292-352.

DR InterPro; IPR009063; Bac_Ig/alg_bind.

DR InterPro; IPR002988; GA.

DR InterPro; IPR005877; Gpos_Y5IRK.

DR InterPro; IPR001899; Gram_pos_anchor.

DR InterPro; IPR000724; IgG_bind_B.

DR Pfam; PF01468; GA; 2.

DR Pfam; PF00746; Gram_pos_anchor; 1.

DR Pfam; PF01378; IgG_binding_B; 2.

DR Pfam; PF04650; Y5IRK_signal; 1.

DR PRINTS; PR00015; GPOSANCHOR.

DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.

DR TIGRFAMS; TIGR01168; Y5IRK_signal; 1.

DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.

KW 3D-structure; Cell wall; IgG-binding protein; Peptidoglycan-anchor;

KW Repeat; Signal.

FT SIGNAL 1 33

FT CHAIN 34 417

FT PROPEP 418 448

FT DOMAIN 69 111

FT DOMAIN 104 215

FT REPEAT 104 140

FT REPEAT 179 215

FT DOMAIN 228 352

FT REPEAT 228 282

FT REPEAT 298 352

FT DOMAIN 386 410

FT SITE 414 418

FT MOD_RES 417 417

FT STRAND 228 234

FT STRAND 239 245

FT HELIX 249 262

FT TURN 263 264

FT STRAND 268 272

FT TURN 273 276

FT STRAND 277 281

FT STRAND 297 304

FT STRAND 309 316

FT HELIX 319 332

FT TURN 333 334

FT STRAND 338 342

FT TURN 343 346

FT STRAND 347 351

SQ SEQUENCE 448 AA; 47567 MW; A0759060C8F9E6CA CRC64;

Query Match 83.6%; Score 281; DB 1; Length 448;

Best Local Similarity 98.2%; Pred. No. 5e-23;

Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TYKLILNGKTLKGETTTEAVDAATAEKVKQYANDNGVDGWTYDDATKTFTVTE 57

Db 228 TYKLILNGKTLKGETTTEAVDAATAEKVKQYANDNGVDGWTYDDATKTFTVTE 282

RESULT 5

Q53337

ID Q53337 PRELIMINARY; PRT; 60 AA.

AC Q53337;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein G IgG Fc binding domain.
GN Name=PGFB;
OS Streptococcus sp. CMCC 32138.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=184480;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCC 32138;
RX MEDLINE=93277681; PubMed=8503988;
RA Cai S.Y., Wang Y.Y., Yao Z.J.;
RT "Structure analysis of streptococcal protein G Fc binding domain.";
RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 36:75-80(1993).
DR EMBL; S62801; AAB27024.1; -.
DR HSSP; P19909; 1P7E.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000724; IGG_bind_B.
DR Pfam; PF01378; IGG_binding_B; 1.
SQ SEQUENCE 60 AA; 6655 MW; 924567E0D6B513DB CRC64;

Query Match 78.6%; Score 264; DB 2; Length 60;
Best Local Similarity 86.0%; Pred. No. 4.8e-22;
Matches 49; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTYDDATKTFVTVE 57
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MTTYKLIVINGKTLKGTTTKTVDAAETAEKAFKQYANDNGVDGVWTYDDATKTFVTVE 57

RESULT 6
Q53974 PRELIMINARY; PRT; 413 AA.
AC Q53974;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mag protein precursor.
GN Name=mag;
OS Streptococcus dysgalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94259307; PubMed=7515368; DOI=10.1016/0378-1119(94)90609-2;
RJ Jonsson H., Frykberg L., Rantamaeki L., Guss B.;
RT "MAG, a novel plasma protein receptor from Streptococcus dysgalactiae";
RL Gene 143:85-89(1994).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
CC EMBL; L27798; AAA26921.1; -.
DR PIR; S55890; S55890.
DR HSSP; P19909; 1P7E.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR009063; Bac_Ig/alb_bind.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; IGG_bind_B.
DR Pfam; PF01468; GA; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; IgG_binding_B; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.

KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 34 Potential.
FT CHAIN 35 413 Potential.
SQ SEQUENCE 413 AA; 44004 MW; F04DC71044F9E50F CRC64;

Query Match 77.7%; Score 261; DB 2; Length 413;
Best Local Similarity 84.2%; Pred. No. 8.1e-21;
Matches 48; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTYDDATKTFVTVE 57
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 256 LTTYKLIVINGKTLKGTTTKAVDAETAETAEKAFKQYANENGVDGVWTYDDATKTFVTVE 312

RESULT 7
Q53975 PRELIMINARY; PRT; 664 AA.
ID Q53975;
AC Q53975; (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Streptococcal surface protein precursor.
GN Name=mig;
OS Streptococcus dysgalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCI;
RX MEDLINE=94192673; PubMed=8143736;
RJ Jonsson H., Mueller H.P.;
RT "The type-III Fc receptor from Streptococcus dysgalactiae is also an alpha-2-macroglobulin receptor.";
RL Eur. J. Biochem. 220:819-826(1994).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
DR EMBL; Z29666; CAA82764.1; -.
DR PIR; S42574; S42574.
DR HSSP; P19909; 1P7E.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; IGG_bind_B.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; IgG_binding_B; 5.
DR Pfam; PF04650; YsIRK_signal; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 664 surface protein.
SQ SEQUENCE 664 AA; 72023 MW; 4A41CEE7977862A CRC64;

Query Match 77.7%; Score 261; DB 2; Length 664;
Best Local Similarity 84.2%; Pred. No. 1.3e-20;
Matches 48; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTYDDATKTFVTVE 57
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 502 LTTYKLIVINGKTLKGTTTKAVDAETAETAEKAFKQYANENGVDGVWTYDDATKTFVTVE 558

RESULT 8
Q93EM8 PRELIMINARY; PRT; 669 AA.
ID Q93EM8

AC Q93EMB; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mig precursor.
OS Streptococcus dysgalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43078;
RX MEDLINE=21437603; PubMed=11553540;
DOI=10.1128/IAI.69.10.6030-6037.2001;
RA Song X.M., Perez-Casal J., Bolton A., Potter A.A.;
RT "Surface-expressed mig protein protects Streptococcus dysgalactiae
against phagocytosis by bovine neutrophils.";
RL Infect. Immun. 69:6030-6037(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43078;
RA Song X.-M., Perez-Casal J., Potter A.A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AF354651; AAL09476.1; -.
DR HSSP; P19909; 1P7E.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR00724; Igg_bind_B.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; Igg_binding_B; 5.
DR Pfam; PF04650; Ysirk_signal; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 39 Potential.
FT CHAIN 40 669 Mig.
SQ SEQUENCE 669 AA; 72681 MW; 5C8982B952029B03 CRC64;

Query Match 76.5%; Score 257; DB 2; Length 669;
Best Local Similarity 82.5%; Pred. No. 3.8e-20;
Matches 47; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTTYKLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTTE 57
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
502 LTTYKLINGKTLKGETTTKAVDVETAETAEKAFKQYANENGVDGWTYDDATKTFVTTE 558

RESULT 9
Q56212 PRELIMINARY; PRT; 429 AA.
AC Q56212;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell surface protein precursor.
OS Streptococcus equi subsp. zooepidemicus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=40041;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=25;
RX MEDLINE=95347809; PubMed=7542636;

RA Jonsson H., Lindmark H., Guss B.;
RT "A protein G-related cell surface protein in Streptococcus
zoepidemicus.";
RL Infect. Immun. 63:2968-2975(1995).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; U25852; AAA86832.1; -.
DR HSSP; P06654; 2IGH.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR009063; Bac_Ig/alb_bind.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; Igg_bind_B.
DR Pfam; PF01468; GA; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; Igg_binding_B; 2.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 33 Potential.
FT CHAIN 34 429 cell surface protein.
SQ SEQUENCE 429 AA; 44830 MW; 270D43F92C197BBA CRC64;

Query Match 65.5%; Score 220; DB 2; Length 429;
Best Local Similarity 70.2%; Pred. No. 3.3e-16;
Matches 40; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTTYKLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTTE 57
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
298 LTTYRLVIKGVTFSGTATKAVDATAETAEQAFRQYANDNGVTGEWAYDAATKTFVTTE 354

RESULT 10
Q76K19 PRELIMINARY; PRT; 433 AA.
AC Q76K19;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cell surface protein.
GN Name=zag;
OS Streptococcus equi subsp. zooepidemicus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=40041;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VTU211;
RA Hong K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AB095372; BAD00711.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR009063; Bac_Ig/alb_bind.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; Igg_bind_B.
DR Pfam; PF01468; GA; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; Igg_binding_B; 2.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.

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DR  TIGRFAMS; TIGR01168; YSIRK signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Peptidoglycan-anchor.
SQ  SEQUENCE 433 AA; 45386 MW; 22F27856AFD752D8 CRC64;

Query Match      65.5%; Score 220; DB 2; Length 433;
Best Local Similarity 68.4%; Pred. No. 3.3e-16;
Matches 39; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY  1 MTTYKLILNGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKTFVTVE 57
    :|||:|:| | ||| :||||| :|:|||||: ||| | |||||
Db  302 LTTYRLVIKGVTFSGETATKAVDAATAEQTFRQYANDNGITGEWAYDTATKTFVTE 358

RESULT 11
Q56192 ID Q56192 PRELIMINARY; PRT; 573 AA.
AC Q56192;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BBM3XM.
GN Name=pSBBM3XM;
OS Staphylococcus xylosus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1288;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92325006; PubMed=1624418;
RA Hansson M., Stahl S., Nguyen T.N., Baechi T., Robert A., Binz H.,
RA Sjoelander A., Uhlen M.;
RT "Expression of recombinant proteins on the surface of the coagulase-
RT negative bacterium Staphylococcus xylosus.";
RL J. Bacteriol. 174:4239-4245(1992).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; M91198; AAA26599.1; -.
DR HSSP; P19909; 1GJT.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0019865; F:immunoglobulin binding; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR InterPro; IPR009063; Bac_Ig/alb_bind.
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; IgG_bind_B.
DR InterPro; IPR002482; LysM.
DR InterPro; IPR005038; Octapeptide.
DR Pfam; PF01468; GA; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; IgG_binding_B; 1.
DR Pfam; PF01476; LysM; 1.
DR GO; GO:0019865; F:immunoglobulin binding; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR InterPro; IPR009063; Bac_Ig/alb_bind.
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; IgG_bind_B.
DR InterPro; IPR002482; LysM.
DR InterPro; IPR005038; Octapeptide.
DR Pfam; PF01468; GA; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; IgG_binding_B; 1.
DR Pfam; PF01476; LysM; 1.
DR Pfam; PF03373; Octapeptide; 13.
DR Pfam; PF04650; YSIRK_signal; 1.
DR ProDom; PD153432; Csurface_antigen; 1.
DR SMART; SM00257; LysM; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 573 AA; 62133 MW; 81E0A458528AEE24 CRC64;

Query Match      38.2%; Score 128.5; DB 2; Length 573;
Best Local Similarity 57.9%; Pred. No. 8.1e-06;
Matches 33; Conservative 1; Mismatches 18; Indels 5; Gaps 2;

QY  3 TYKLILNGKTLKGETTTEAVDAATAAKV-FKQYANDNGVDGEWYDDATKTFVTTEH 58
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  238 TYKLILNGKTLKGETTTEAVDAATAARSFNFPILENSSSVPG----DPLESTCMHVEH 290
```

```
RESULT 12
Q56193 ID Q56193 PRELIMINARY; PRT; 492 AA.
AC Q56193;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BBXM.
GN Name=pSBBmp18XM;
OS Staphylococcus xylosus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1288;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92325006; PubMed=1624418;
RA Hansson M., Stahl S., Nguyen T.N., Baechi T., Robert A., Binz H.,
RA Sjoelander A., Uhlen M.;
RT "Expression of recombinant proteins on the surface of the coagulase-
RT negative bacterium Staphylococcus xylosus.";
RL J. Bacteriol. 174:4239-4245(1992).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; M91199; AAA26600.1; -.
DR HSSP; P19909; 1GJT.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0019865; F:immunoglobulin binding; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR InterPro; IPR009063; Bac_Ig/alb_bind.
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; IgG_bind_B.
DR InterPro; IPR002482; LysM.
DR InterPro; IPR005038; Octapeptide.
DR Pfam; PF01468; GA; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; IgG_binding_B; 1.
DR Pfam; PF01476; LysM; 1.
DR Pfam; PF03373; Octapeptide; 13.
DR Pfam; PF04650; YSIRK_signal; 1.
DR ProDom; PD153432; Csurface_antigen; 1.
DR SMART; SM00257; LysM; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 492 AA; 52708 MW; 6581D37EED16952B CRC64;

Query Match      37.9%; Score 127.5; DB 2; Length 492;
Best Local Similarity 69.0%; Pred. No. 9e-06;
Matches 29; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY  3 TYKLILNGKTLKGETTTEAVDAATAAKV-FKQYANDNGVDGE 43
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  238 TYKLILNGKTLKGETTTEAVDAATAARSFNFPILENSSSVPGD 279

RESULT 13
Q8RYL7 ID Q8RYL7 PRELIMINARY; PRT; 412 AA.
AC Q8RYL7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE OSJNBa0052012.3 protein (OSJNBa0093F16.27 protein).
GN Name=OSJNBa0052012.3; Synonyms=OSJNBa0093F16.27;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
```


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OM protein - protein search, using sw model

Run on: August 9, 2005, 10:10:50 ; Search time 39 Seconds
(without alignments)
152.960 Million cell updates/sec

Title: US-10-672-108-6
Perfect score: 336
Sequence: 1 MTTYKLILNGKTLKGTTTE.....EWTYDDATKTFTVTEHHHHH 62

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	285	84.8	455	2	A45063	immunoglobulin-bin
2	284	84.5	593	2	S00128	protein G precursor
3	281	83.6	448	2	A24496	IgG-binding protei
4	261	77.7	413	2	S55890	plasma protein rec
5	261	77.7	664	2	S42574	streptococcal surf
6	74	22.0	1965	2	S75200	fat protein - Syne
7	68	20.2	1020	2	D83679	hypothetical prote
8	64.5	19.2	148	2	S70733	ferric uptake tran
9	64.5	19.2	148	2	AE0321	ferric uptake regu
10	64.5	19.2	737	1	S14408	translation elonga
11	64	19.0	1081	2	T31094	surface antigen Bs
12	63.5	18.9	308	2	H81345	hypothetical prote
13	63	18.8	148	2	D89973	hypothetical prote
14	63	18.8	1347	2	T30909	endo-1,4-beta-xyla
15	62.5	18.6	148	2	B90718	negative regulator
16	62.5	18.6	148	2	S07308	ferric uptake tran
17	62.5	18.6	148	2	B85568	negative regulator
18	62.5	18.6	150	2	AB0586	ferric uptake regu
19	62.5	18.6	260	2	T18909	hypothetical prote
20	62.5	18.6	296	2	I40267	outer surface prot
21	61.5	18.3	640	2	A41726	homeotic protein B
22	61.5	18.3	642	2	S27806	homeotic protein B
23	61.5	18.3	736	1	S31809	translation elonga
24	61.5	18.3	1156	2	T23308	hypothetical prote
25	61	18.2	148	2	G83681	urease accessory p
26	61	18.2	248	2	AI2703	prokaryotic type I
27	61	18.2	248	2	A97486	prokaryotic type I
28	61	18.2	831	2	T00323	chitinase (EC 3.2.
29	61	18.2	1902	2	B45764	lactocepin (EC 3.4

30	61	18.2	2334	2	S32920	cell wall-associat
31	60.5	18.0	504	2	S33188	phase-1 flagellin
32	60.5	18.0	504	2	S33187	phase-1 flagellin
33	60.5	18.0	507	2	S33185	phase-1 flagellin
34	60.5	18.0	979	2	G81103	type III restricti
35	60.5	18.0	26926	1	I38344	titin, cardiac mus
36	60	17.9	136	2	T22959	hypothetical prote
37	60	17.9	215	2	AG3011	ATP-dependent prot
38	60	17.9	230	2	H98272	ATP-dependent prot
39	60	17.9	331	1	S69190	myb-related protei
40	60	17.9	382	2	S13237	tail fiber protein
41	60	17.9	520	2	T20007	hypothetical prote
42	60	17.9	1356	2	S51389	ROM2 protein - yea
43	59.5	17.7	212	2	S35268	glutathione transf
44	59.5	17.7	358	2	A89980	hypothetical prote
45	59.5	17.7	476	2	T47941	hypothetical prote

ALIGNMENTS

RESULT 1

A45063
immunoglobulin-binding protein LG - Peptostreptococcus magnus
C;Species: Peptostreptococcus magnus
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
C;Accession: A45063
R;Kihlberg, B.M.; Sjobring, U.; Kastern, W.; Bjorck, L.
J. Biol. Chem. 267, 25583-25588, 1992
A;Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties.
A;Reference number: A45063; MUID:93094283; PMID:1460053
A;Accession: A45063
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-455 <KIH>
A;Cross-references: GB:S50809; NID:g261705; PIDN:AAA03280.1; PID:g261706
A;Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBIIP:120303)

Query Match 84.8%; Score 285; DB 2; Length 455;
Best Local Similarity 96.5%; Pred. No. 3e-24;
Matches 55; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKTFTVTE 57

Db 328 MDTYKLILNGKTLKGTTTEAVDAATAEKVFKQYANDNGVDGEWYDDATKTFTVTE 384

RESULT 2

S00128
protein G precursor - Streptococcus sp. (Streptococcus G148)
N;Alternate names: albumin-binding protein; cell wall-bound protein
C;Species: Streptococcus sp.
A;Variety: Streptococcus G148
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00128; A27604; A26314
R;Olsson, A.; Eliasson, M.; Guss, B.; Nilsson, B.; Hellman, U.; Lindberg, M.; Uhlen, M.
Eur. J. Biochem. 168, 319-324, 1987
A;Title: Structure and evolution of the repetitive gene encoding streptococcal protein
A;Reference number: S00128; MUID:88029445; PMID:3665928
A;Accession: S00128
A;Molecule type: DNA
A;Residues: 1-593 <OLS>
A;Cross-references: UNIPROT:P19909; EMBL:X06173; NID:g47084; PIDN:CAA29540.1; PID:g4708
A;Note: the source is designated as Streptococcus G148
A;Note: part of this sequence, including the amino end of the mature protein, was confi
R;Sjoebbring, U.; Falkenberg, C.; Nielsen, E.; Akerstroem, B.; Bjoerck, L.
J. Immunol. 140, 1595-1599, 1988
A;Title: Isolation and characterization of a 14-kDa albumin-binding fragment of strepto
A;Reference number: A27604; MUID:88154455; PMID:2831269
A;Accession: A27604
A;Molecule type: protein
A;Residues: 62-101 <SJO>
R;Guss, B.; Eliasson, M.; Olsson, A.; Uhlen, M.; Frej, A.K.; Jornvall, H.; Flock, J.I.;

EMBO J. 5, 1567-1575, 1986
A;Title: Structure of the IgG-binding regions of streptococcal protein G.
A;Reference number: A26314; MUID:86300657; PMID:3017704
A;Accession: A26314
A;Molecule type: DNA
A;Residues: 114-593 <GUS>
A;Cross-references: GB:X04015; NID:g47071; PIDN:CAA27638.1; PID:g47072
C;Function:
A;Description: it is part of the cell wall structure of group G streptococci and is cova
C;Superfamily: M5 protein
C;Keywords: duplication; membrane protein
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-593/Product: protein G #status experimental <MAT>
F;34-116/Domain: alanine-rich <ALA>
F;117-290/Domain: AB duplication <DUP1>
F;117-140/Region: A repeat
F;141-191/Region: B
F;192-215/Region: A repeat
F;216-266/Region: B
F;267-290/Region: A repeat
F;303-497/Domain: IgG binding <IGB>
F;303-357/Region: C repeat
F;358-372/Region: D
F;373-427/Region: C repeat
F;428-442/Region: D
F;443-497/Region: C repeat
F;498-567/Domain: proline-rich <PRO>
F;568-593/Domain: carboxyl-terminal <CTD>

Query Match 84.5%; Score 284; DB 2; Length 593;
Best Local Similarity 93.0%; Pred. No. 5.2e-24;
Matches 53; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTYDDATKTFVTVE 57
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 371 VTTYKLIVINGKTLKGTTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFVTVE 427

RESULT 3
A24496
IgG-binding protein - Streptococcus sp. (group G)
C;Species: Streptococcus sp.
C;Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 09-Jul-2004
C;Accession: A24496; A39041
R;Fahnestock, S.R.; Alexander, P.; Nagle, J.; Filpula, D.
J. Bacteriol. 167, 870-880, 1986
A;Title: Gene for an immunoglobulin-binding protein from a group G Streptococcus.
A;Reference number: A24496; MUID:86304178; PMID:3745123
A;Accession: A24496
A;Molecule type: DNA
A;Residues: 1-448 <FAH>
A;Cross-references: UNIPROT:P06654; GB:M13825; NID:g153822; PIDN:AAA03664.1; PID:g153823
R;Sjoebing, U.; Bjoerck, L.; Kastern, W.
J. Biol. Chem. 266, 399-405, 1991
A;Title: Streptococcal protein G. Gene structure and protein binding properties.
A;Reference number: A39041; MUID:91093154; PMID:1985908
A;Accession: A39041
A;Status: preliminary
A;Molecule type: protein
A;Residues: 34-42,'N',45-48;62-76;186-200 <SJO>
C;Genetics:
A;Gene: spg
C;Superfamily: M5 protein
C;Keywords: transmembrane protein

Query Match 83.6%; Score 281; DB 2; Length 448;
Best Local Similarity 98.2%; Pred. No. 8.3e-24;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTYDDATKTFVTVE 57
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 228 TYKLILNGKTLKGTTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFVTVE 282

RESULT 4
S55890
plasma protein receptor MAG precursor - Streptococcus dysgalactiae
C;Species: Streptococcus dysgalactiae
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55890
R;Jonsson, H.; Frykberg, L.; Rantamaeki, L.; Guss, B.
Gene 143, 85-89, 1994
A;Title: MAG, a novel plasma protein receptor from Streptococcus dysgalactiae.
A;Reference number: S55890; MUID:94259307; PMID:7515368
A;Accession: S55890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-413 <JON>
A;Cross-references: UNIPROT:Q53974; EMBL:L27798; NID:g475117; PIDN:AAA26921.1; PID:g4751
C;Superfamily: M5 protein

Query Match 77.7%; Score 261; DB 2; Length 413;
Best Local Similarity 84.2%; Pred. No. 1.3e-21;
Matches 48; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTYDDATKTFVTVE 57
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 256 LTTYKLIVINGKTLKGTTTKAVDAETAEKAFKQYANENGVDGVWTYDDATKTFVTVE 312

RESULT 5
S42574
streptococcal surface protein - Streptococcus dysgalactiae
C;Species: Streptococcus dysgalactiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S42574
R;Jonsson, H.; Mueller, H.P.
Eur. J. Biochem. 220, 819-826, 1994
A;Title: The type-III Fc receptor from Streptococcus dysgalactiae is also an alpha(2)-ma
A;Reference number: S42574; MUID:94192673; PMID:8143736
A;Accession: S42574
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-664 <JON>
A;Cross-references: UNIPROT:Q53975; EMBL:Z29666; NID:g470220; PIDN:CAA82764.1; PID:g4702
C;Superfamily: M5 protein

Query Match 77.7%; Score 261; DB 2; Length 664;
Best Local Similarity 84.2%; Pred. No. 2.2e-21;
Matches 48; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTYDDATKTFVTVE 57
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 502 LTTYKLIVINGKTLKGTTTKAVDAETAEKAFKQYANENGVDGVWTYDDATKTFVTVE 558

RESULT 6
S75200
fat protein - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein slr2046
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75200
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
S.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75200
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1965 <KAN>
A;Cross-references: UNIPROT:P73089; EMBL:D90903; GB:AB001339; NID:g1652127; PIDN:BAA1711
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Db | : || : | : | : : : | : | : ||
48 BEIGLATVYRVLNQF-DDAGIVTRHNFEGGKSVFELTQQHHH 88

Search completed: August 9, 2005, 10:21:08
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: August 9, 2005, 10:07:30 ; Search time 161 Seconds
(without alignments)
148.939 Million cell updates/sec

Title: US-10-672-108-6
Perfect score: 336
Sequence: 1 MTTYKLILNGKTLKGETTE.....EWTYDDATKTFTVTEHHHH 62

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336	100.0	62	4 AAB30886	Aab30886 Amino aci
2	332	98.8	62	4 AAB30894	Aab30894 Amino aci
3	331	98.5	62	4 AAB30925	Aab30925 Amino aci
4	331	98.5	62	4 AAB30926	Aab30926 Amino aci
5	331	98.5	62	4 AAB30883	Aab30883 Amino aci
6	326	97.0	62	4 AAB30885	Aab30885 Amino aci
7	325	96.7	62	4 AAB30891	Aab30891 Amino aci
8	325	96.7	62	4 AAB30888	Aab30888 Amino aci
9	325	96.7	62	4 AAB30887	Aab30887 Amino aci
10	323	96.1	62	4 AAB30884	Aab30884 Amino aci
11	323	96.1	62	4 AAB30890	Aab30890 Amino aci
12	323	96.1	62	4 AAB30889	Aab30889 Amino aci
13	317	94.3	62	4 AAB30892	Aab30892 Amino aci
14	317	94.3	62	4 AAB30893	Aab30893 Amino aci
15	285	84.8	434	2 AAR42994	Aar42994 Sequence
16	284	84.5	61	2 AAW44390	Aaw44390 Protein G
17	284	84.5	64	2 AAW44395	Aaw44395 Protein G
18	284	84.5	78	2 AAR11382	Aar11382 Fc-bindin
19	284	84.5	78	2 AAR11383	Aar11383 Fc-bindin
20	284	84.5	185	3 AAY57610	Aay57610 Streptoco
21	284	84.5	228	3 AAB10433	Aab10433 Expressio
22	284	84.5	250	3 AAB10434	Aab10434 Expressio
23	284	84.5	269	2 AAR53295	Aar53295 Igg-bindi
24	284	84.5	402	2 AAW21716	Aaw21716 RIP fusio
25	284	84.5	402	2 AAW25129	Aaw25129 Pro-ribos

26	284	84.5	480	1 AAP70468	Aap70468 Sequence
27	284	84.5	489	2 AAR20085	Aar20085 Maize RIP
28	284	84.5	489	2 AAW21717	Aaw21717 RIP fusio
29	284	84.5	489	2 AAW25130	Aaw25130 Pro-ribos
30	284	84.5	493	2 AAW21719	Aaw21719 RIP fusio
31	284	84.5	493	2 AAW25132	Aaw25132 Pro-ribos
32	284	84.5	502	2 AAW21720	Aaw21720 RIP fusio
33	284	84.5	502	2 AAW25133	Aaw25133 Pro-ribos
34	284	84.5	593	2 AAR62944	Aar62944 Streptoco
35	282	83.9	607	2 AAR91016	Aar91016 PRSVPGclu
36	282	83.9	611	2 AAR91018	Aar91018 PRSVFGLcl
37	281	83.6	55	6 ABR43647	Abr43647 Streptoco
38	281	83.6	55	8 ADO39742	Ado39742 Protein G
39	281	83.6	55	8 ADR49519	Adr49519 Staphyloc
40	281	83.6	55	8 ADR49521	Adr49521 Streptoco
41	281	83.6	56	4 AAE07440	Aae07440 Streptoco
42	281	83.6	56	6 ABU12183	Abu12183 Immunoglo
43	281	83.6	57	2 AAW44389	Aaw44389 Protein G
44	281	83.6	131	1 AAP94791	Aap94791 Protein G
45	281	83.6	131	2 AAR07008	Aar07008 Protein G

ALIGNMENTS

RESULT 1
AAB30886
ID AAB30886 standard; protein; 62 AA.

XX AC AAB30886;
XX DT 02-APR-2001 (first entry)
XX DE Amino acid sequence of a B1 domain of protein G with mutation E27A.
XX KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
XX KW knobs-into-holes binding site.
XX OS Synthetic.
XX OS Streptococcus sp.
XX FH Key Location/Qualifiers
FT Misc-difference 28 /note= "Glu changed to Ala"
XX FT
XX PN WO200074728-A1.
XX PD 14-DEC-2000.

XX 02-JUN-2000; 2000WO-US015366.
XX PR 04-JUN-1999; 99US-00326342.
XX PA (UYDU-) UNIV DUKE.
XX PI Hellinga HW, Sloan DJ;
XX DR WPI; 2001-049994/06.
XX DR N-PSDB; AAC86821.

XX B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.

XX Claim 7; Page 73; 83pp; English.

XX The present sequence represents a mutated B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu27 residue of the mature B1 domain acts as a charged knob on the
CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A

CC mutation of this residue virtually abolishes stable complex formation.
CC The B1 domain can be immobilized to a solid phase support, and be used
CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
CC by affinity chromatography. The B1 domain is also useful for detecting
CC IgG or its fragments in a clinical sample
XX
SQ Sequence 62 AA;

Query Match 100.0%; Score 336; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.5e-34;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTDYDDATKTFVTVEHHH 60
|||
Db 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTDYDDATKTFVTVEHHH 60
|||

QY 61 HH 62
||
Db 61 HH 62

RESULT 2
AAB30894
ID AAB30894 standard; protein; 62 AA.
XX
AC AAB30894;
XX
DT 02-APR-2001 (first entry)
XX
DE Amino acid sequence of a mutated B1 domain of protein G.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.
XX
OS Synthetic.
OS Streptococcus sp.
XX
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX
DR WPI; 2001-049994/06.
DR N-PSDB; AAC86827.
XX
PT B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.
XX
PS Claim 7; Page 79; 83pp; English.
XX
CC The present sequence represents a mutated B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu27 residue of the mature B1 domain acts as a charged knob on the
CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A
CC mutation of this residue virtually abolishes stable complex formation.
CC The B1 domain can be immobilized to a solid phase support, and be used
CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
CC by affinity chromatography. The B1 domain is also useful for detecting
CC IgG or its fragments in a clinical sample
XX
SQ Sequence 62 AA;

Query Match 98.8%; Score 332; DB 4; Length 62;
Best Local Similarity 98.4%; Pred. No. 1.4e-33;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTDYDDATKTFVTVEHHH 60
|||
Db 1 MTTYKLILNGKTLKGTTTEAVDAATAVFKQYANDNGVDGEWTDYDDATKTFVTVEHHH 60
|||

QY 61 HH 62
||
Db 61 HH 62

RESULT 3
AAB30925
ID AAB30925 standard; protein; 62 AA.
XX
AC AAB30925;
XX
DT 02-APR-2001 (first entry)
XX
DE Amino acid sequence of a mutated B1 domain of protein G.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.
XX
OS Synthetic.
OS Streptococcus sp.
XX
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX
DR WPI; 2001-049994/06.
DR N-PSDB; AAC86828.
XX
PT B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.
XX
PS Claim 7; Page 80; 83pp; English.
XX
CC The present sequence represents a mutated B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu27 residue of the mature B1 domain acts as a charged knob on the
CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A
CC mutation of this residue virtually abolishes stable complex formation.
CC The B1 domain can be immobilized to a solid phase support, and be used
CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
CC by affinity chromatography. The B1 domain is also useful for detecting
CC IgG or its fragments in a clinical sample
XX
SQ Sequence 62 AA;

Query Match 98.5%; Score 331; DB 4; Length 62;
Best Local Similarity 98.4%; Pred. No. 1.9e-33;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTDYDDATKTFVTVEHHH 60
|||
Db 1 MTTYKLILNGKTLKGTTTEAVDAATALKVFKQYANDNGVDGEWTDYDDATKTFVTVEHHH 60
|||

Qy 61 HH 62
Db 61 HH 62

RESULT 4

AAB30926
ID AAB30926 standard; protein; 62 AA.

XX AC AAB30926;

XX DT 02-APR-2001 (first entry)

DE Amino acid sequence of a mutated B1 domain of protein G.

XX KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.

XX OS Synthetic.

OS Streptococcus sp.

XX PN WO200074728-A1.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-US015366.

XX PR 04-JUN-1999; 99US-00326342.

XX PA (UYDU-) UNIV DUKE.

XX PI Hellinga HW, Sloan DJ;

XX DR WPI; 2001-049994/06.

DR N-PSDB; AAC86829.

XX PT B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.

XX PS Claim 7; Page 81; 83pp; English.

XX CC The present sequence represents a mutated B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu27 residue of the mature B1 domain acts as a charged knob on the
CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A
CC mutation of this residue virtually abolishes stable complex formation.
CC The B1 domain can be immobilized to a solid phase support, and be used
CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
CC by affinity chromatography. The B1 domain is also useful for detecting
CC IgG or its fragments in a clinical sample

XX SQ Sequence 62 AA;

Query Match 98.5%; Score 331; DB 4; Length 62;
Best Local Similarity 98.4%; Pred. No. 1.9e-33;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTTYKLILNGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKTFTVTEHHH 60
Db 1 MTTYKLILNGKTLKGETTTEAVDAATAIKVFKQYANDNGVDGEWYDDATKTFTVTEHHH 60

Qy 61 HH 62
Db 61 HH 62

RESULT 5

AAB30883
ID AAB30883 standard; protein; 62 AA.

XX AAB30883;
XX DT 02-APR-2001 (first entry)

XX DE Amino acid sequence of the native B1 domain of protein G.

XX KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.

XX OS Streptococcus sp.

XX FH Key Location/Qualifiers

FT Protein 2.62

FT /note= "mature protein"

XX PN WO200074728-A1.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-US015366.

XX PR 04-JUN-1999; 99US-00326342.

XX PA (UYDU-) UNIV DUKE.

XX PI Hellinga HW, Sloan DJ;

XX DR WPI; 2001-049994/06.

DR N-PSDB; AAC86820.

XX PT B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.

XX PS Disclosure; Page 50; 83pp; English.

XX CC The present sequence represents a native B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu27 residue of the mature B1 domain acts as a charged knob on the
CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A
CC mutation of this residue virtually abolishes stable complex formation.
CC The B1 domain can be immobilized to a solid phase support, and be used
CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
CC by affinity chromatography. The B1 domain is also useful for detecting
CC IgG or its fragments in a clinical sample

XX SQ Sequence 62 AA;

Query Match 98.5%; Score 331; DB 4; Length 62;
Best Local Similarity 98.4%; Pred. No. 1.9e-33;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTTYKLILNGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKTFTVTEHHH 60
Db 1 MTTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWYDDATKTFTVTEHHH 60

Qy 61 HH 62
Db 61 HH 62

RESULT 6

AAB30885
ID AAB30885 standard; protein; 62 AA.

XX AC AAB30885;

XX DT 02-APR-2001 (first entry)

DE Amino acid sequence of a B1 domain of protein G with mutation T25A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.
XX
OS Synthetic.
OS Streptococcus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 26 /note= "mature protein"
FT
FT Misc-difference 26 /note= "wild type Thr changed to Ala"
FT
XX
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX
DR WPI; 2001-049994/06.
XX
PS B1 domain polypeptide of bacterial protein G, useful for detection and
XX purification of antibody fragments, exhibits binding activity for Fab
XX fragment of an IgG but does not bind Fc fragment.
XX
XX Example 1; Page 72; 83pp; English.
XX
CC The present sequence represents a mutated B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu28 residue of the B1 domain acts as a charged knob on the surface of
CC the B1 domain, inserting a polar hole on the Fc fragment. A mutation of
CC this residue virtually abolishes stable complex formation. The B1 domain
CC can be immobilized to a solid phase support, and be used for purifying Fc
CC and Fab fragments of IgG from a warm-blooded vertebrate by affinity
CC chromatography. The B1 domain is also useful for detecting IgG or its
CC fragments in a clinical sample
XX
SQ Sequence 62 AA;

Query Match 97.0%; Score 326; DB 4; Length 62;
Best Local Similarity 96.8%; Pred. No. 7.9e-33;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWTDATKTFVTEHHH 60
|||
Db 1 MTTYKLILNGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWTDATKTFVTEHHH 60
|||
QY 61 HH 62
||
Db 61 HH 62

RESULT 7
AAB30891
ID AAB30891 standard; protein; 62 AA.
XX
AC AAB30891;
XX
DT 02-APR-2001 (first entry)
XX
DE Amino acid sequence of a B1 domain of protein G with mutation E42A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;

KW knobs-into-holes binding site.
XX
OS Synthetic.
OS Streptococcus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 43 /note= "Glu changed to Ala"
FT
XX
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX
DR WPI; 2001-049994/06.
XX
PS B1 domain polypeptide of bacterial protein G, useful for detection and
XX purification of antibody fragments, exhibits binding activity for Fab
XX fragment of an IgG but does not bind Fc fragment.
XX
PS Disclosure; Page 76; 83pp; English.
XX
CC The present sequence represents a mutated B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu27 residue of the mature B1 domain acts as a charged knob on the
CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A
CC mutation of this residue virtually abolishes stable complex formation.
CC The B1 domain can be immobilized to a solid phase support, and be used
CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
CC by affinity chromatography. The B1 domain is also useful for detecting
CC IgG or its fragments in a clinical sample
XX
SQ Sequence 62 AA;

Query Match 96.7%; Score 325; DB 4; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.1e-32;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWTDATKTFVTEHHH 60
|||
Db 1 MTTYKLILNGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWTDATKTFVTEHHH 60
|||
QY 61 HH 62
||
Db 61 HH 62

RESULT 8
AAB30888
ID AAB30888 standard; protein; 62 AA.
XX
AC AAB30888;
XX
DT 02-APR-2001 (first entry)
XX
DE Amino acid sequence of a B1 domain of protein G with mutation K31A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.
XX
OS Synthetic.
OS Streptococcus sp.
XX

FH Key Location/Qualifiers
FT Misc-difference 32
FT /note= "Lys changed to Ala"
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX
XX WPI; 2001-049994/06.
DR N-PSDB; AAC86823.
XX
PT B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.
XX
PS Claim 7; Page 75; 83pp; English.
XX
XX The present sequence represents a mutated B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu27 residue of the mature B1 domain acts as a charged knob on the
CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A
CC mutation of this residue virtually abolishes stable complex formation.
CC The B1 domain can be immobilized to a solid phase support, and be used
CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
CC by affinity chromatography. The B1 domain is also useful for detecting
CC IgG or its fragments in a clinical sample
XX
SQ Sequence 62 AA;

Query Match 96.7%; Score 325; DB 4; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.1e-32;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKFTVTTEHHH 60
|||
Db 1 MTTYKLILNGKTLKGTTTEAVDAATAEKVFAQYANDNGVDGEWYDDATKFTVTTEHHH 60

QY 61 HH 62
||
Db 61 HH 62

RESULT 9
AAB30887
ID AAB30887 standard; protein; 62 AA.
XX
AC AAB30887;
XX
DT 02-APR-2001 (first entry)
XX
DE Amino acid sequence of a B1 domain of protein G with mutation K28A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.
XX
OS Synthetic.
OS Streptococcus sp.
XX
XX Key Location/Qualifiers
FT Misc-difference 29
FT /note= "Lys changed to Ala"
XX

PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX
XX WPI; 2001-049994/06.
DR N-PSDB; AAC86822.
XX
PT B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.
XX
PS Claim 7; Page 74; 83pp; English.
XX
XX The present sequence represents a mutated B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu27 residue of the mature B1 domain acts as a charged knob on the
CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A
CC mutation of this residue virtually abolishes stable complex formation.
CC The B1 domain can be immobilized to a solid phase support, and be used
CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
CC by affinity chromatography. The B1 domain is also useful for detecting
CC IgG or its fragments in a clinical sample
XX
SQ Sequence 62 AA;

Query Match 96.7%; Score 325; DB 4; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.1e-32;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKFTVTTEHHH 60
|||
Db 1 MTTYKLILNGKTLKGTTTEAVDAATAEAVFKQYANDNGVDGEWYDDATKFTVTTEHHH 60

QY 61 HH 62
||
Db 61 HH 62

RESULT 10
AAB30884
ID AAB30884 standard; protein; 62 AA.
XX
AC AAB30884;
XX
DT 02-APR-2001 (first entry)
XX
DE Amino acid sequence of a B1 domain of protein G with mutation Q32C.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.
XX
OS Synthetic.
OS Streptococcus sp.
XX
XX Key Location/Qualifiers
FT Protein 2..62
FT /note= "mature protein"
FT Misc-difference 33
FT /note= "wild type Gln changed to Cys"
XX
PN WO200074728-A1.
XX

PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX
DR WPI; 2001-049994/06.
XX
XX B1 domain polypeptide of bacterial protein G, useful for detection and purification of antibody fragments, exhibits binding activity for Fab fragment of an IgG but does not bind Fc fragment.
PS Example 1; Page 72; 83pp; English.
XX
CC The present sequence represents a mutated B1 domain of the bacterial protein G. The B1 domain exhibits binding activity for a Fab fragment of an immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment of an IgG. The B1 domain may further comprise a disrupted or mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu28 residue of the B1 domain acts as a charged knob on the surface of the B1 domain, inserting a polar hole on the Fc fragment. A mutation of this residue virtually abolishes stable complex formation. The B1 domain can be immobilized to a solid phase support, and be used for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate chromatography. The B1 domain is also useful for detecting IgG or its fragments in a clinical sample
XX
SQ Sequence 62 AA;

Query Match 96.1%; Score 323; DB 4; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.9e-32;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKFTVTEHHH 60
Db 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKFTVTEHHH 60

QY 61 HH 62
Db 61 HH 62

RESULT 11
AAB30890
ID AAB30890 standard; protein; 62 AA.
XX
AC AAB30890;
XX
DT 02-APR-2001 (first entry)
XX
DE Amino acid sequence of a B1 domain of protein G with mutation D40A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.
XX
OS Synthetic.
OS Streptococcus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 41 /note= "Asp changed to Ala"
FT
XX
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX

XX (UYDU-) UNIV DUKE.
PA
XX Hellinga HW, Sloan DJ;
PI
XX WPI; 2001-049994/06.
DR
XX
XX B1 domain polypeptide of bacterial protein G, useful for detection and purification of antibody fragments, exhibits binding activity for Fab fragment of an IgG but does not bind Fc fragment.
PT
PT
XX
PS Disclosure; Page 76; 83pp; English.
XX
CC The present sequence represents a mutated B1 domain of the bacterial protein G. The B1 domain exhibits binding activity for a Fab fragment of an immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment of an IgG. The B1 domain may further comprise a disrupted or mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu27 residue of the mature B1 domain acts as a charged knob on the surface of the B1 domain, inserting a polar hole on the Fc fragment. A mutation of this residue virtually abolishes stable complex formation. The B1 domain can be immobilized to a solid phase support, and be used for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate by affinity chromatography. The B1 domain is also useful for detecting IgG or its fragments in a clinical sample
XX
SQ Sequence 62 AA;

Query Match 96.1%; Score 323; DB 4; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.9e-32;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKFTVTEHHH 60
Db 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVAGEWYDDATKFTVTEHHH 60

QY 61 HH 62
Db 61 HH 62

RESULT 12
AAB30889
ID AAB30889 standard; protein; 62 AA.
XX
AC AAB30889;
XX
DT 02-APR-2001 (first entry)
XX
DE Amino acid sequence of a B1 domain of protein G with mutation N35A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.
XX
OS Synthetic.
OS Streptococcus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 35 /note= "Asn changed to Ala"
FT
XX
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX

DR WPI; 2001-049994/06.
DR N-PSDB; AAC86824.
XX
PT B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.
XX
PS Claim 7; Page 76; 83pp; English.
XX
CC The present sequence represents a mutated B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu27 residue of the mature B1 domain acts as a charged knob on the
CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A
CC mutation of this residue virtually abolishes stable complex formation.
CC The B1 domain can be immobilized to a solid phase support, and be used
CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
CC by affinity chromatography. The B1 domain is also useful for detecting
CC IgG or its fragments in a clinical sample
XX
SQ Sequence 62 AA;

Query Match 96.1%; Score 323; DB 4; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.9e-32;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTEHHH 60
|||
Db 1 MTTYKLILNGKTLKGETTTEAVDAATAAEKVFKQYAADNGVDGWTYDDATKTFVTEHHH 60

QY 61 HH 62
||
Db 61 HH 62

RESULT 13
AAB30892
ID AAB30892 standard; protein; 62 AA.
AC AAB30892;
XX
XX 02-APR-2001 (first entry)
DT
DE Amino acid sequence of a B1 domain of protein G with mutation W43A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.
XX
OS Synthetic.
OS Streptococcus sp.
XX
XX Key Location/Qualifiers
FT Misc-difference 44 /note= "Trp changed to Ala"
FT
XX WO200074728-A1.
PN
XX 14-DEC-2000.
PD
XX 02-JUN-2000; 2000WO-US015366.
PF
XX 04-JUN-1999; 99US-00326342.
PR
XX (UYDU-) UNIV DUKE.
PA
XX Hellinga HW, Sloan DJ;
PI
XX WPI; 2001-049994/06.
DR N-PSDB; AAC86825.
DR
XX B1 domain polypeptide of bacterial protein G, useful for detection and

PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.
XX
PS Claim 23; Page 77; 83pp; English.
XX
CC The present sequence represents a mutated B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu27 residue of the mature B1 domain acts as a charged knob on the
CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A
CC mutation of this residue virtually abolishes stable complex formation.
CC The B1 domain can be immobilized to a solid phase support, and be used
CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
CC by affinity chromatography. The B1 domain is also useful for detecting
CC IgG or its fragments in a clinical sample
XX
SQ Sequence 62 AA;

Query Match 94.3%; Score 317; DB 4; Length 62;
Best Local Similarity 96.8%; Pred. No. 1e-31;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTEHHH 60
|||
Db 1 MTTYKLILNGKTLKGETTTEAVDAATAAEKVFKQYANDNGVDGWTYDDATKTFVTEHHH 60

QY 61 HH 62
||
Db 61 HH 62

RESULT 14
AAB30893
ID AAB30893 standard; protein; 62 AA.
XX
AC AAB30893;
XX
XX 02-APR-2001 (first entry)
DT
DE Amino acid sequence of a B1 domain of protein G with mutation T44A/Y45A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site.
XX
OS Synthetic.
OS Streptococcus sp.
XX
XX Key Location/Qualifiers
FT Misc-difference 45 /note= "Thr changed to Ala"
FT Misc-difference 46 /note= "Tyr changed to Ala"
FT
XX WO200074728-A1.
PN
XX 14-DEC-2000.
PD
XX 02-JUN-2000; 2000WO-US015366.
PF
XX 04-JUN-1999; 99US-00326342.
PR
XX (UYDU-) UNIV DUKE.
PA
XX Hellinga HW, Sloan DJ;
PI
XX WPI; 2001-049994/06.
DR N-PSDB; AAC86826.
DR
XX B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.

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XX PS Claim 27; Page 78; 83pp; English.
XX CC The present sequence represents a mutated B1 domain of the bacterial
CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
CC fragment of an IgG. The B1 domain may further comprise a disrupted or
CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
CC Glu27 residue of the mature B1 domain acts as a charged knob on the
CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A
CC mutation of this residue virtually abolishes stable complex formation.
CC The B1 domain can be immobilized to a solid phase support, and be used
CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
CC by affinity chromatography. The B1 domain is also useful for detecting
CC IgG or its fragments in a clinical sample
XX SQ Sequence 62 AA;

Query Match 94.3%; Score 317; DB 4; Length 62;
Best Local Similarity 95.2%; Pred. No. 1e-31;
Matches 59; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGWTYYDDATKTFVTEHHH 60
Db 1 MTTYKLILNGKTLKGTTTEAVDAATAEKVFKQYANDNGVDGEWAADDAATKTFVTEHHH 60

QY 61 HH 62
Db 61 HH 62

RESULT 15
AAR42994
ID AAR42994 standard; protein; 434 AA.
XX AC AAR42994;
XX DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-MAY-1994 (first entry)
XX DE Sequence encoding immunoglobulin light chain binding protein.
XX KW Immunoglobulin; light chain; binding; identification; purification;
KW separation; ss.
XX OS Escherichia coli.
XX FH Key Location/Qualifiers
FT Domain 5..305
FT /label= B1 immunoglobulin light chain binding domain.
FT Domain 81..305
FT /label= B2 immunoglobulin light chain binding domain.
FT Domain 153..305
FT /label= B3 immunoglobulin light chain binding domain.
FT Domain 225..305
FT /label= B4 immunoglobulin light chain binding domain.
FT Domain 297..305
FT /label= B5 immunoglobulin light chain binding domain.
FT Domain 309..434
FT /label= C1 immunoglobulin heavy chain binding domain.
FT Domain 364..434
FT /label= D intermediate immunoglobulin heavy chain binding
FT domain.
FT Domain 379..434
FT /label= C2 immunoglobulin heavy chain binding domain.
XX PN WO9322342-A1.
XX PD 11-NOV-1993.
XX PF 28-APR-1993; 93WO-SE000375.
XX XX
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PR 28-APR-1992; 92SE-00001331.
XX (HIGH-) HIGHTECH RECEPTOR AB.
XX Bjoerck L, Sjoebbring U;
XX WPI; 1993-368722/46.
XX P-PSDB; AAR42994.
XX New protein L binding light chains of all immunoglobulin classes - for
PT binding purifying and identifying immunoglobulin, also related DNA,
PT vectors and host cells.
XX Claim 6; Page 39-40; 71pp; English.
XX Protein L (AAR42993) is capable of binding to immunoglobulin G light
CC chains. It is useful for binding, separating (purifying) and identifying
CC immunoglobulin and for removing immunoglobulin molecules from serum. This
CC is the coding sequence of one hybrid protein of the L protein. The hybrid
CC proteins can bind all human immunoglobulin classes and many
CC immunoglobulins from other species. They are highly soluble and retain
CC their binding activity at high temperatures over a pH range of 3-10. They
CC can be immobilised without loss of activity. (Updated on 25-MAR-2003 to
CC correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 434 AA;

Query Match 84.8%; Score 285; DB 2; Length 434;
Best Local Similarity 96.5%; Pred. No. 1.2e-26;
Matches 55; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTTYKLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGWTYYDDATKTFVTE 57
Db 307 MDTYKLILNGKTLKGTTTEAVDAATAEKVFKQYANDNGVDGWTYYDDATKTFVTE 363

Search completed: August 9, 2005, 10:17:23
Job time : 163 secs
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